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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 9, 2002, 01:39:36 ; Search time 2215 Seconds
(without alignments)
4167.687 Million cell updates/sec

Title: US-09-895-298A-32_COPY_63_632
Perfect score: 570

Sequence: 1 atgatgaattccagcctcc.....aagaaggtatccaagggcc 570

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
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11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_trod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568.4	99.7	807	12	BG184448 RST3374 A
2	565.8	99.3	777	12	BG217799 RST37513
3	554.4	97.3	691	10	AW582253 QV4-ST021
4	543.6	95.4	768	12	BG194960 RST14018
5	535.4	93.9	789	12	BG221275 RST41079
6	530	93.0	837	12	BG216071 RST35885

7	523.6	91.9	810	12	BG217267	BG217267 RST36969
8	523.6	91.9	823	12 <th>BG183902</th> <th>BG183902 RST2815 A</th>	BG183902	BG183902 RST2815 A
9	467.8	82.1	698	12 <th>BF375244</th> <th>BF375244 QV4-ST021</th>	BF375244	BF375244 QV4-ST021
10	445.4	78.1	822	12 <th>BG219307</th> <th>BG219307 RST39061</th>	BG219307	BG219307 RST39061
11	442.2	77.6	871	12 <th>BG198917</th> <th>BG198917 RST18188</th>	BG198917	BG198917 RST18188
12	434	76.1	2721	11 <th>AK016573</th> <th>AK016573 Mus muscu</th>	AK016573	AK016573 Mus muscu
13	411.6	72.2	758	12 <th>BG198969</th> <th>BG198969 RST18241</th>	BG198969	BG198969 RST18241
14	401.4	70.4	447	13 <th>BG982234</th> <th>BG982234 CM4-CN008</th>	BG982234	BG982234 CM4-CN008
15	338.8	59.4	594	10 <th>AW469181</th> <th>AW469181 hc78f11.x</th>	AW469181	AW469181 hc78f11.x
16	299	52.5	558	10 <th>AW469177</th> <th>AW469177 hc78e12.x</th>	AW469177	AW469177 hc78e12.x
17	294.8	51.7	558	9 <th>A1799626</th> <th>A1799626 to74b03.x</th>	A1799626	A1799626 to74b03.x
18	286.6	50.3	855	12 <th>BG204090</th> <th>BG204090 RST23484</th>	BG204090	BG204090 RST23484
19	268	47.0	376	12 <th>BE849364</th> <th>BE849364 uw88h05.y</th>	BE849364	BE849364 uw88h05.y
20	268	47.0	491	10 <th>AW913564</th> <th>AW913564 uf54e02.y</th>	AW913564	AW913564 uf54e02.y
21	251.8	44.2	508	12 <th>BF375243</th> <th>BF375243 QV4-ST021</th>	BF375243	BF375243 QV4-ST021
22	242.8	42.6	829	12 <th>BG201350</th> <th>BG201350 RST20811</th>	BG201350	BG201350 RST20811
23	229.4	40.2	565	14 <th>BQ552730</th> <th>BQ552730 H4017G07-</th>	BQ552730	BQ552730 H4017G07-
24	219.8	38.6	307	12 <th>BG187692</th> <th>BG187692 RST6558 A</th>	BG187692	BG187692 RST6558 A
25	215.4	37.8	480	9 <th>A1697014</th> <th>A1697014 wc76h09.x</th>	A1697014	A1697014 wc76h09.x
26	210	36.8	415	14 <th>BQ084432</th> <th>BQ084432 K-EST0149</th>	BQ084432	BQ084432 K-EST0149
27	210	36.8	482	14 <th>BM773483</th> <th>BM773483 K-EST0057</th>	BM773483	BM773483 K-EST0057
28	203.6	35.7	398	14 <th>BM773482</th> <th>BM773482 K-EST0057</th>	BM773482	BM773482 K-EST0057
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30	186.8	32.8	529	13 <th>BM432955</th> <th>BM432955 LJE38B4.a</th>	BM432955	BM432955 LJE38B4.a
31	182.4	32.0	268	12 <th>BG184955</th> <th>BG184955 RST3889 A</th>	BG184955	BG184955 RST3889 A
32	174.4	30.6	428	9 <th>A1830044</th> <th>A1830044 w58f02.x</th>	A1830044	A1830044 w58f02.x
33	168.8	29.6	846	12 <th>BG202006</th> <th>BG202006 RST21353</th>	BG202006	BG202006 RST21353
34	165	28.9	639	14 <th>BM978431</th> <th>BM978431 UI-CE-DU1</th>	BM978431	BM978431 UI-CE-DU1
35	155.8	27.3	243	12 <th>BG216765</th> <th>BG216765 RST36460</th>	BG216765	BG216765 RST36460
36	150	26.3	191	9 <th>AA371314</th> <th>AA371314 EST83087</th>	AA371314	AA371314 EST83087
37	139.6	24.5	652	9 <th>AV226010</th> <th>AV226010 AV226010</th>	AV226010	AV226010 AV226010
38	122.4	21.5	359	14 <th>BM750790</th> <th>BM750790 K-EST0026</th>	BM750790	BM750790 K-EST0026
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ALIGNMENTS

RESULT 1
BG184448

LOCUS BG184448 807 bp mRNA EST 21-ADR-2001

DEFINITION RST3374 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
ACCESSION BG184448
VERSION BG184448.1 GI:13706135

KEYWORDS

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
'Lerner,L., Costanzo,D., McElligott,K., Boozar,S., Mays,R., Smith,
'E., Veloso,N., Klitka,A., Hess,J., Colhren,K., Lo,K., Offenbacher,
'J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random
activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE

JOURNAL

MEDLINE

COMMENT

Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@atersys.com

High quality sequence stop: 499.

Location/Qualifiers

FEATURES

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1. .807
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="See 'Creation of Genome-wide Protein Expression
libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT      211 a      195 c      178 g      222 t
ORIGIN

Query Match      99.7%; Score 568.4; DB 12; Length 807;
Best Local Similarity 99.8%; Pred. No. 8.4e-151;
Matches 569; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGATGAATTTCCACCTCCGAGCAAAAGCCTGGCGGCTTCACAGATGATGACTTCTTC 60
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QY 181 TCCATCTACAGCTGGATCGACACCCCTAAGTACACGGCTGCTACCTGTGGTGTGG 240
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Db 625 AGATCAGTTCAAGAAGTAATCCAAAGGCC 654

RESULT 2
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LOCUS      BG217799
DEFINITION  RST37513 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG217799
VERSION    BG217799.1 GI:13743820
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 777)
            Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.
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lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
,E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher
,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 512.

FEATURES
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Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT      196 a      193 c      173 g      214 t
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Matches 567; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 ATCTTCTGCTCTTTTCCATCTTTACACCGGGCTCTTGACACCTGGCCATCACCATC 120
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QY 241 ATCTATCGGAACCTTCATTTGAGTGTGACCTTTTTCATCTCCTCACTCATTTGTGCTA 300
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LOCUS      AM582253                691 bp    mRNA    linear    EST 16-MAR-2000
DEFINITION QV4-ST0212-120100-075-f09 ST0212 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AM582253
VERSION     AM582253.1  GI:7257302
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 691)
AUTHORS     HCGP http://www.ludwig.org.br/ORESTES.
TITLE       The FAPESP/LICR Human Cancer Genome Project
JOURNAL     Unpublished (1999)
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV4&t2=QV4-ST0212-
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            Site_2: SmaI; A mini-library was made by cloning products
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            profiles into the pUC 18 vector. Reverse transcription of
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BASE COUNT  179 a      167 c      157 g      188 t
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Query Match      97.3%; Score 554.4; DB 10; Length 691;
Best Local Similarity 99.5%; Pred. No. 7.8e-147;
Matches 567; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

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RESULT 4
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LOCUS      BG194960                768 bp    mRNA    linear    EST 21-APR-2001
DEFINITION RST14018 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION  BG194960
VERSION     BG194960.1  GI:13716535
KEYWORDS   EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 768)
AUTHORS     Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
            Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
            ,E., Veloso,N., Rlika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
            ,J., Danzig,J. and Ducar,M.
            Creation of genome-wide protein expression libraries using random
            activation of gene expression
            Nat. Biotechnol. 19 (5), 440-445 (2001)
            21227151
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scai@atersys.com
            High quality sequence stop: 469.
FEATURES
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            method was used, these sequence tags are not necessarily
            expressed in HT1080 under normal circumstances."
BASE COUNT  197 a      188 c      171 g      212 t
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Best Local Similarity 98.2%; Pred. No. 9.5e-144;
Matches 560; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

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QY 121 TGGAGATTGAAGCCTTACGCTGACTGTGGCCCTTTTCGAGTCTGCGCTCTCTTCATTGAC 180
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QY 241 ATCTATCGGAACCTCATTTGGAAGTGTGCACTTCTTTTCATCCTCAACCTCATTTGTGCTA 300
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Db 325 ATCTATCGGAACCTCATTTGGAAGTGTGCACTTCTTTTCATCCTCAACCTCATTTGTGCTA 384
QY 301 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGAGATTATGATAAGGCTGCTC 360
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Db 385 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGAGATTATGATAAGGCTGCTC 444
QY 361 CATGAGCAGATCATTTATGAGGCGCAAGATAAATGTCTCTGATAGAAAAATGATCAAG 420
|||||
Db 445 CATGAGCAGATCATTTATGAGGCGCAAGATAAATGTCTCTGATAGAAAAATGATCAAG 504
QY 421 CTCGAGATATGAGAGAAAGCAACCCAGCTCCTGTCTGGAAGAGAGAGAGTGTG 480
|||||
Db 505 CTCGAGATATGAGAGAAAGCAACCCAGCTCCTGTCTGGAAGAGAGAGAGTGTG 564
QY 481 GAGCAACAAGCCTTTTTCATTTGGGGGACATATGAGCTTGTACTTGGCATCTAGA 540
|||||
Db 565 GAGCAACAAGCCTTTTTCATTTGGGGGACATATGAGCTTGTACTTGGCATCTAGA 624
QY 541 AGATCAGTTCAAGAAGGTATATCCAAAGGCC 570
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Db 625 AGA-CAGTTCAAGAAGGTATATCCAAAGGCC 653

RESULT 5

Bg221275

LOCUS

DEFINITION RST41079 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
Bg221275

ACCESSION

VERSION Bg221275.1 GI:13747296

KEYWORDS

EST.

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 789)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,
J., Danzig,J. and Ducar,M.

TITLE

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL

MEDLINE

COMMENT

CONTACT: Scott J. Cain

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Fax: 216 361 9596

Email: scai@atersys.com

High quality sequence stop: 533.

FEATURES

Source

location/Qualifiers

1..789

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Athersys RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression

Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the

cell type indicated is HT1080, since a random activation

method was used, these sequence tags are not necessarily

BASE COUNT 191 a 194 c 171 g 226 t 7 others
ORIGIN

Query Match 93.9%; Score 535.4; DB 12; Length 789;
Best Local Similarity 97.0%; Pred. No. 2.1e-141;
Matches 553; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 1 ATGATGAATTTCACGCTCCGAGCAAAAGCCTGGCGGCTCACAGATGATGACTTCTTC 60
|||||
Db 188 ATGATGAATTTCACGCTCCGAGCAAAAGCCTGGCGGCTCACAGATGATGACTTCTTC 247
QY 61 ATCTTCTGCTCTTTTCCATCTTTCACCGGGGCTTGTGCACCTGGCCATCACCATC 120
|||||
Db 248 ATCTTCTGCTCTTTTCCATCTTTCACCGGGGCTTGTGCACCTGGCCATCACCATC 307
QY 121 TGGAGATTGAAGCCTTACGCTGACTGTGGCCCTTTTCGAGTCTGCGCTCTCTTCATTGAC 180
|||||
Db 308 TGGAGATTGAAGCCTTACGCTGACTGTGGCCCTTTTCGAGTCTGCGCTCTCTTCATTGAC 367
QY 181 TCCATCTACAGCTGGATCGACACCCCTAAGTACACGGCCCTGCTACCTGTGGTGTGG 240
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Db 368 TCCATCTACAGCTGGATCGACACCCCTAAGTACACGGCCCTGCTACCTGTGGTGTGG 427
QY 241 ATCTATCGGAACCTCATTTGGAAGTGTGCACTTCTTTTCATCCTCAACCTCATTTGTGCTA 300
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Db 428 ATCTATCGGAACCTCATTTGGAAGTGTGCACTTCTTTTCATCCTCAACCTCATTTGTGCTA 487
QY 301 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGAGATTATGATAAGGCTGCTC 360
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Db 488 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGAGATTATGATAAGGCTGCTC 547
QY 361 CATGAGCAGATCATTTATGAGGCGCAAGATAAATGTCTCTGATAGAAAAATGATCAAG 420
|||||
Db 548 CATGAGCAGATCATTTATGAGGCGCAAGATAAATGTCTCTGATAGAAAAATGATCAAG 607
QY 421 CTCGAGATATGAGAGAAAGCAACCCAGCTCCTGTCTGGAAGAGAGAGAGTGTG 480
|||||
Db 608 CTCGAGATATGAGAGAAAGCAACCCAGCTCCTGTCTGGAAGAGAGAGAGTGTG 667
QY 481 GAGCAACAAGCCTTTTTCATTTGGGGGACATATGAGCTTGTACTTGGCATCTAGA 540
|||||
Db 668 GAGCAACAAGCCTTTTTCATTTGGGGGACATATGAGCTTGTACTTGGCATCTAGA 726
QY 541 AGATCAGTTCAAGAAGGTATATCCAAAGGCC 570
|||||
Db 727 AGATCAGTTCAAGAAGGTATATCCAAAGGCC 756

RESULT 6

Bg216071

LOCUS

DEFINITION RST35885 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
Bg216071

ACCESSION

VERSION Bg216071.1 GI:13742220

KEYWORDS

EST.

SOURCE

ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 837)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,
J., Danzig,J. and Ducar,M.

TITLE

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL

MEDLINE

COMMENT

CONTACT: Scott J. Cain

ATHERSYS, INC.
3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900
Fax: 216 361 9596

Email: scain@ethersys.com

High quality sequence stop: 537.

FEATURES

source

Location/Qualifiers

1. 837

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Athersys RAGE Library"

/cell_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 208 a 209 c 184 g 235 t 1 others

ORIGIN

Query Match

93.0%; Score 530; DB 12; Length 837;

Best Local Similarity 97.9%; Pred. No. 7.2e-140;

Matches 558; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

OY 1 ATGATGATTTCCAGCCTCCGAGCAAGCCCTGGCGCTCAGAGATGATCTTCTC 60
|||||
DB 124 ATGATGATTTCCAGCCTCCGAGCAAGCCCTGGCGCTCAGAGATGATCTTCTC 183
|||||
OY 61 ATCTCTTGCTCTTTTCCATCTTTCACCGGGGCTGTGACACCTGGCCATCACCATC 120
|||||
DB 184 ATCTCTTGCTCTTTTCCATCTTTCACCGGGGCTGTGACACCTGTCTTTCACCATC 243
|||||
OY 121 TGGAGATGAGCCTTCAGCTGAGTGGCCCTTTTGAGAGTGTGCTCTCTTCATTCAC 180
|||||
DB 244 TGGAGATGAGCCTTCAGCTGAGTGGCCCTTTTGAGAGTGTGCTCTCTTCATTCAC 303
|||||
OY 181 TCCATCTACAGCTGGATGACACACCCTAAGTACACGGCCTGCTACCTGTGGGTGTTGG 240
|||||
DB 304 TCCATCTACAGCTGGATGACACACCCTAAGTACACGGCCTGCTACCTGTGGGTGTTGG 363
|||||
OY 241 ATCTATCGGAACCTCATTTGGAAGTGTGACCTTTTTCATCTCACCCTCATTTGCTA 300
|||||
DB 364 ATCTATCGGAACCTCATTTGGAAGTGTGACCTTTTTCATCTCACCCTCATTTGCTA 423
|||||
OY 301 ATCATCACTATCTTACTGGCAGATCACAGAGGGAAGATTAATGATTAAGGCTGCTC 360
|||||
DB 424 ATCATCACTATCTTACTGGCAGATCACAGAGGGAAGATTAATGATTAAGGCTGCTC 483
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OY 361 CATGACGAGATCAATTAATGAGGCAAGATTAATGCTCTGATAGAAAAATTGATCAAG 420
|||||
DB 484 CATGACGAGATCAATTAATGAGGCAAGATTAATGCTCTGATAGAAAAATTGATCAAG 543
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OY 421 CTGACAGATATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAGAGAGAGGTG 480
|||||
DB 544 CTGACAGATATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAGAGAGAGGTG 603
|||||
OY 481 GAGCAACAAGGCTTTTGGATTTGGGGGAACATGATGGCAGTCTTGACTTGCATAGAGA 540
|||||
DB 604 GAGC-ACAAGGCTTTTGGATTTGGGGGAACATGATGGCAG-CTTGACTTGGGATCTAGA 661
|||||
OY 541 AGATCAGTTCAAGAAGGTAATCCAAAGGCC 570
|||||
DB 662 AGATCAGTTCAAGAAGGTAATCCAAAGGCC 691
|||||

RESULT 7

BG217267

LOCUS BG217267 810 bp mRNA linear EST 21-APR-2001

DEFINITION RST36969 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG217267

VERSION BG217267.1 GI:13743288

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,

Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.

Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith

J., Veloso, N., Klika, A., Hess, J., Colgren, K., Lo, K., Offenbacher

J., Danzig, J., and Ducar, M.

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

21227151

Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@ethersys.com

High quality sequence stop: 466.

FEATURES

source

Location/Qualifiers

1. 810

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Athersys RAGE Library"

/cell_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 207 a 196 c 180 g 227 t

ORIGIN

Query Match

91.9%; Score 523.6; DB 12; Length 810;

Best Local Similarity 96.3%; Pred. No. 4.7e-138;

Matches 547; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

OY 1 ATGATGATTTCCAGCCTCCGAGCAAGCCCTGGCGCTCAGAGATGATGATCTTCTC 60
|||||
DB 85 ATGATGATTTCCAGCCTCCGAGCAAGCCCTGGCGCTCAGAGATGATGATCTTCTC 144
|||||
OY 61 ATCTCTTGCTCTTTTCCATCTTTCACCGGGGCTGTGACACCTGGCCATCACCATC 120
|||||
DB 145 ATCTCTTGCTCTTTTCCATCTTTCACCGGGGCTGTGACACCTGGCCATCACCATC 204
|||||
OY 121 TGGAGATGAGCCTTCAGCTGAGTGGCCCTTTTGAGAGTGTGCTCTCTTCATTCAC 180
|||||
DB 205 TGGAGATGAGCCTTCAGCTGAGTGGCCCTTTTGAGAGTGTGCTCTCTTCATTCAC 264
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OY 181 TCCATCTACAGCTGGATGACACACCCTAAGTACACGGCCTGCTACCTGTGGGTGTTGG 240
|||||
DB 265 TCCATCTACAGCTGGATGACACACCCTAAGTACACGGCCTGCTACCTGTGGGTGTTGG 324
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OY 241 ATCTATCGGAACCTCATTTGGAAGTGTGACCTTTTTCATCTCACCCTCATTTGCTA 300
|||||
DB 325 ATCTATCGGAACCTCATTTGGAAGTGTGACCTTTTTCATCTCACCCTCATTTGCTA 384
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OY 301 ATCATCACTATCTTACTGGCAGATCACAGAGGGAAGATTAATGATTAAGGCTGCTC 360
|||||
DB 385 ATCATCACTATCTTACTGGCAGATCACAGAGGGAAGATTAATGATTAAGGCTGCTC 444
|||||
OY 361 CATGACGAGATCAATTAATGAGGCAAGATTAATGCTCTGATAGAAAAATTGATCAAG 420
|||||
DB 445 CATGACGAGATCAATTAATGAGGCAAGATTAATGCTCTGATAGAAAAATTGATCAAG 504
|||||
OY 421 CTGACAGATATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAGAGAGAGGTG 480
|||||
DB 505 CTGACAGATATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAGAGAGAGGTG 564
|||||
OY 481 GAGCAACAAGGCTTTTGGATTT- -GGGGAACATGATGGCAGTCTGACTTGGCATCTA 538
|||||
DB 565 GAGCAACAAGGCTTTTGGATTTTGAAGGGAACATGATGGCAGTCTGACTTGGCATCTA 624
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QY      539 GAAGATCAGTTCAAGAGTAATCCAG 566
Db      625 GAAATCAATTCAGAGGAAATCCAGG 652

RESULT 8
LOCUS    Bg183902
DEFINITION RST2815 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION Bg183902
VERSION   Bg183902.1 GI:13705589
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 823)
AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
           Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
           Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith
           ,E., Veloso,N., Klika,A., Hess,J., Cochren,K., Lo,K., Offenbacher
           ,J., Danzig,J. and Ducar,M.
           Creation of genome-wide protein expression libraries using random
           activation of gene expression
           Nat. Biotechnol. 19 (5), 440-445 (2001)
JOURNAL   21227151
MEDLINE
COMMENT    Contact: Scott J. Cain
           Athersys, Inc.
           3201 Carnegie Ave, Cleveland, OH 44115, USA
           Tel: 216 431 9900
           Fax: 216 361 9596
           Email: scaina@athersys.com
           High quality sequence stop: 449.
           Location/Qualifiers
FEATURES
     source             1..823
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone_lib="Athersys RAGE Library"
                        /note="See 'Creation of Genome-wide Protein Expression
                        Libraries using Random Activation of Gene Expression',
                        Nature Biotechnology, in press. Note that even though the
                        cell type indicated is HT1080, since a random activation
                        method was used, these sequence tags are not necessarily
                        expressed in HT1080 under normal circumstances."
BASE COUNT  211 a      203 c      180 g      229 t
ORIGIN
Query Match          91.9%; Score 523.6; DB 12; Length 823;
Best Local Similarity 97.2%; Pred. No. 4.7e-138;
Matches 554; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

QY      1 ATGATGAATTTTCAGCCTCGAGCAAAAGCCTGGCGGCTTCACAGATGATGACTTTCTTC 60
Db      109 ATGATGAATTTTCAGCCTCGAGCAAAAGCCTGGCGGCTTCACAGATGATGACTTTCTTC 168

QY      61 ATCTTCTGCTCTTTTCCATCTTTTACCGGGGCTTGTGCACCTGGCCATCACCATC 120
Db      169 ATCTTCTGCTCTTTTCCATCTTTTACCGGGGCTTGTGCACCTGGCCATCACCATC 228

QY      121 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTGAAGTCTGCCTCTTCATTCAC 180
Db      229 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTGAAGTCTGCCTCTTCATTCAC 288

QY      181 TCCATCTACAGCTGGATGCACACCCCTAAGTACACGGCCGTGCTGAGGCTGTGTTGG 240
Db      289 TCCATCTACAGCTGGATGCACACCCCTAAGTACACGGCCGTGCTGAGGCTGTGTTGG 348

QY      241 ATCTATCGGAACCTTATTTGAAGTGTGCACTTTTTCATCTCCTGACCCCTCATTTGTGCTA 300
Db      349 ATCTATCGGAACCTTATTTGAAGTGTGCACTTTTTCATCTCCTGACCCCTCATTTGTGCTA 408

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```

QY      301 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGAGATTATGATAAGCCTGCTC 360
Db      409 ATCATCACCTATCTTTACTGGCAGATCACAGAGGGAAGAGATTATGATAAGCCTGCTC 468

QY      361 CATGAGCAGATCATTAATGAGGGCAAAAGATTAATGTTCTCGATAGAAAAATTGATCAAG 420
Db      469 CATGAGCAGATCATTAATGAGGGCAAAAGATTAATGTTCTCGATAGAAAAATTGATCAAG 528

QY      421 CTCGAGATATGAGAGAAAGCAAAACCCAGCTCATTGTTCTGGAAAGAGAGAGCTG 480
Db      529 CTCGAGATATGAGAGAAAGCAAAACCCAGCTCATTGTTCTGGAAAGAGAGAGGCTG 588

QY      481 G-AGCAACAAGGCTTTTTCATTTGGGGGAACATGATGCGAGTCTTGACTTGCATCTAG 539
Db      589 GAAGCAACAAGGCTTTTTCATTTGGGGGAACATGATGCGAGTCTTGACTTGCATCTAA 647

QY      540 AAGATCAGTTCAAGAGTAATCCAGGCG 569
Db      648 AATATCAGTTCAAGAGTAATCCAGGCGC 677

RESULT 9
LOCUS    BF375244
DEFINITION QV4-ST0212-261199-045-c09 ST0212 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF375244
VERSION   BF375244.1 GI:11337269
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 698)
AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Bionesi,M.R.,
           Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
           Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
           Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
           ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
           Simpson,A.J.
           Shotgun sequencing of the human transcriptome with ORF expressed
           sequence tags
           Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL   20202663
MEDLINE
COMMENT    Contact: Simpson A.J.G.
           Laboratory of Cancer Genetics
           Ludwig Institute for Cancer Research
           Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
           Brazil
           Tel: +55-11-2704922
           Fax: +55-11-2707001
           Email: asimpson@ludwig.org.br
           This sequence was derived from the FAPESP/LICR Human Cancer Genome
           project. This entry can be seen in the following URL
           (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&lt2=QV4-ST0212-
           261199-045-c09&lt3=1999-11-26&lt4=1)
           Seq primer: puc 18 forward
           High quality sequence start: 14
           High quality sequence stop: 36.
           Location/Qualifiers
FEATURES
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                        /db_xref="taxon:9606"
                        /clone_lib="ST0212"
                        /dev_stage="Adult"
                        /note="Organ: stomach; Vector: puc18; Site_1: Smal;
                        Site_2: SmaI; A mini-library was made by cloning products
                        derived from ORESTES PCR (U.S. Letters Patent application
                        No. 196,716 - Ludwig Institute for Cancer Research)
                        profiles into the pUC 18 vector. Reverse transcription of
                        tissue mRNA and cDNA amplification were performed under
                        low stringency conditions."
BASE COUNT  177 a      173 c      164 g      184 t
ORIGIN

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Query Match	82.1%;	Score 467.8;	DB 12;	Length 698;
Best Local Similarity	-93.4%;	Pred. No. 3.4e-122;		
Matches 522;	Conservative 0;	Mismatches 32;	Indels 5;	Gaps 3

OY	16	CCTCCAGCAAAACGCTGGCGGGCCCTACAGA----	TGATGACTTTCCTCATCTTCTTGCTC	72
Db	46	CGTCAGTAGCAAGCCGTGGCGGCCCTAACAGACGATAGACTTTCTATCATCTTCTGCTC		105
OY	73	T-TTTTTCCCATTCTTTTACCAGGGGGTCTTGTCACCCCTGGCCATCACCATCTGGAGATTGAA		131
Db	106	TATTTTCCATCTCTTACCCGGGGTCTTGTCACCCCTGGCCATCACCATCTGGAGATTGAA		165
OY	132	GCCCTTCAGCTGCATGTGGCCCTTTTCGAGGTCTGCCTCTCTCATTCACCTCCATCTACAG		191
Db	166	GCCCTTCACCTGCATGTGGCCCTTTTCGAGGTCTGCCTCTCTCATTCACCTCCATCTACAG		225
OY	192	CTGGATCGACACCCCTAAGTAACACGCGCTGGCTACCTGTGGGTGTTTGGATCTATCGGAA		251
Db	226	CTGGATCGACACCCCTAAGTAACACGCGCTGGCTACCTGTGGGTGTTTGGATCTATCGGAA		285
OY	252	CCCTCATTTGGAAGTGTGCACCTTCTTTTCATCCTCACCCCTCATTTGTGCTAATCATCACCTA		311
Db	286	CCCTCATTTGGAAGTGTGCACCTTCTTTTCATCCTCACCCCTCATTTGTGCTAATCATCACCTA		345
OY	312	TCTTTACTGGCAGATCACAGAGGGAAGAAATTATGATTAAGCTGCTCCATGAGCAGAT		371
Db	346	TCTTTACTGGCAGATCACAGAGGGAAGAAATTATGATTAAGCTGCTCCATGAGCAGAT		405
OY	372	CATTATATGAGGGCAAAGATAAAATGTTCTCTGATAGAAAAATTGATCAAGCTGCAGGATAT		431
Db	406	CATTATATGAGGGCAAAGATCAAAATGTTCTCTGATAGAAAACAATTGATCAAGCTGCAGGATAT		465
OY	432	GGAGAAGAAAGCAAAACCCACAGCTCACTGTGTCGGAAGAGAGAGAGGTGGAGCAACAAGG		491
Db	466	GGCGACGACCGCAAA-CCACAGCTCACTGTGTCGGAAGAGAGAGAGGTGGAGCAACAAGG		524
OY	492	CTTTTTCATTTGGGGGAACATGATGGCAGTCTTGACTTGGCATCTAGAAAGATCAGTTCA		551
Db	525	CTTATTTGCATTTAGCCGGGAACATGATGGCAGTCTTGACTTGGCATCTAGACGATCAGTTCA		584
OY	552	AGAAGGTAATCCAAGGGCC	570	
Db	585	AGAAGGTAATCCAAGGGCC	603	

BESULT	10
LOCUS	BG219307
DEFINITION	BG219307 822 bp mRNA linear EST 21-APR-2001 RST39061 Athersys RAGE Library Homo sapiens cdNA, mRNA sequence.
ACCESSION	BG219307
VERSION	BG219307.1 GI:13745328
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 822)
AUTHORS	Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith, 'E., Veloso,N., Kilka,A., Hess,J., Cothren,K., Lo,K., Offenbacher ,J., Danzig,J. and Ducar,M. Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001) 21227151
TITLE	Contact: Scott J. Cain
JOURNAL	Athersys, Inc.
MEDLINE	3201 Carnegie Ave, Cleveland, OH 44115, USA
COMMENT	Tel: 216 431 9900 Fax: 216 361 9596 Email: scaina@aterssys.com

High quality sequence stop: 473	
Location/Qualifiers	
1. .822	
source	
FEATURES	

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology', in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT      241 a      169 c      179 g      230 t
ORIGIN

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Query Match	78.1%;	Score 445.4;	DB 12;	Length 822;
Best Local Similarity	99.8%;	Pred. No. 8.5e-116;		
Matches 446; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

OY	124	AGATTGAAGCCTTCAAGCTGACGTGCGCCCTTTTCGAGGCTGCCTCTCTCATTCACCTCC	183
Db	76	ATATTGAAGCCTTCAAGCTGACGTGCGCCCTTTTCGAGGCTGCCTCTCTCATTCACCTCC	135
OY	184	ATCTACAGCTGGATGACGACACCCTTAAGTACAACGCCCTGGCTACTCTGTGGCTTTGGATC	243
Db	136	ATCTACAGCTGGATGACGACACCCTTAAGTACAACGCCCTGGCTACTCTGTGGCTTTGGATC	195
OY	244	TATCGGAACCTCATGCGAAGTGTCGACTTCTTTTCATCCTCACCCCTCATTTGTGCTAATC	303
Db	196	TATCGGAACCTCATGCGAAGTGTCGACTTCTTTTCATCCTCACCCCTCATTTGTGCTAATC	255
OY	304	ATCACTATCTTTACTGGCAGATCACAGAGGGAAGAAGATTATGATAAGCTGCTCCAT	363
Db	256	ATCACTATCTTTACTGGCAGATCACAGAGGGAAGAAGATTATGATAAGCTGCTCCAT	315
OY	364	GAGCAGATCATTAATGAGGGCAAAGATAAATGTTCTGATAGAAAAATTGATCAAAGCTG	423
Db	316	GAGCAGATCATTAATGAGGGCAAAGATAAATGTTCTGATAGAAAAATTGATCAAAGCTG	375
OY	424	CAGGATATGGAGAAGAAAACCAACCCGCTCACTGTCTCTGGAAGGAGAGAGGTGGAG	483
Db	376	CAGGATATGGAGAAGAAAACCAACCCGCTCACTGTCTCTGGAAGGAGAGAGGTGGAG	435
OY	484	CAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGCTTGACTTGCGATCTTAGAAGA	543
Db	436	CAACAAGGCTTTTTGCATTTGGGGGAACATGATGGCAGCTTGACTTGCGATCTTAGAAGA	495
OY	544	TCAGTTCAAGAAGGTAAATCCAAGGGCC	570
Db	496	TCAGTTCAAGAAGGTAAATCCAAGGGCC	522

[illegible]

MEDLINE		21227151	
COMMENT	Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 44115, USA Tel: 216 431 9900 Fax: 216 361 9596 Email: scain@athersys.com High quality sequence stop: 498. Location/Qualifiers 1. 871 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Athersys RAGE Library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances." BASE COUNT 252 a 186 c 185 g 246 t ORIGIN Query Match 77.6%; Score 442.2; DB 12; Length 871; Best Local Similarity 99.3%; Pred. No. 7e-115; Matches 444; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
FEATURES	source 1. 871 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Athersys RAGE Library" /cell_line="HT1080" /note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances." BASE COUNT 252 a 186 c 185 g 246 t ORIGIN		
LOCUS	AK016573 2721 bp mRNA linear HTC 19-JAN-2002		
DEFINITION	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932443L08; homolog to CDNA FLJ13553 FIS, CLONE PLACE1009493, full insert sequence.		
ACCESSION	AK016573		
VERSION	AK016573.1 GI:12855380		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone:4932443L08.		
ORGANISM	Mus musculus		

BASE COUNT 172 a 193 c 163 g 229 t 1 others
ORIGIN

Query Match 72.2%; Score 411.6; DB 12; Length 758;
Best Local Similarity 96.4%; Pred. No. 3.5e-106;
Matches 453; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

QY 1 ATGATGAATTTCCAGCCTCCGACCAAGCCTGGCGCTCAGAGATGATGACTTCTTC 60
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QY 121 TGGAGATGGAAGCCTTCAGCTGAGCTGTGGCCCTTTTCGAGGTCTGCTCTTCATTTCAC 180
DB 404 TGGAGATGGAAGCCTTCAGCTGAGCTGTGGCCCTTTTCGAGGTCTGCTCTTCATTTCAC 463
QY 181 TCCATCTACAGCTGGATGACACACCTTAAGTACACGCGCTGCTACCTGTGGGTGTTGG 240
DB 464 TCCATCTACAGCTGGATGACACACCTTAAGTACACGCGCTGCTACCTGTGGGTGTTGG 523
QY 241 ATCTATCGGAACCTCATTTGGAGCTGTGACTCTTTTTCATCTCTACCCCTCATTTGCTCA 300
DB 524 ATCTATCGGAACCTCATTTGGAGCTGTGACTCTTTTTCATCTCTACCCCTCATTTGCTCA 583
QY 301 ATCATCACCTATCTTTACTGCGAGATCAGAGGGAAGGAAATTATGATTAAGGCTGCTC 360
DB 584 ATCATCACCTATCTTTACTGCGAGATCAGAGGGAAGGAAATTATGATTAAGGCTGCTC 643
QY 361 CATGAGCAGATCATTTATGAGGCAAAAGATTAATGTTCTGATAGAAAATGATCAAG 420
DB 644 C-TTAGCAGATCATTTATGAGGCAAAATTAATGTTCTGATGCAATTA-TGATCAAG 701
QY 421 CTGCGAGATGATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAG 470
DB 702 CTGCGAGATGATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAAG 750

RESULT 14
BG982234/c 447 bp mRNA linear EST 12-JUN-2001
LOCUS BG982234
DEFINITION CM4-CN0089-130201-723-e04 CN0089 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG982234
VERSION BG982234.1 GI:14384969
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 447)

TITLE
JOURNAL
MEDLINE
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4<2=CM4-CN0089-130201-723-e04<3=2001-02-13<4=1)
Seq primer: puc 18 forward
High quality sequence start: 25
High quality sequence stop: 447.
Location/Qualifiers
1. 447

FEATURES
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/db_xref="taxon:9606"
/clone_lib="CN0089"
/dev_stage="Adult"
/note="Organ: colon_normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 114 a 107 c 95 g 131 t
ORIGIN

Query Match 70.4%; Score 401.4; DB 13; Length 447;
Best Local Similarity 99.8%; Pred. No. 2.4e-103;
Matches 402; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 168 TCTCTTCATTCACCTCCATCTACAGCTGATGACACCCCTAAGTACACGGCTGCTACCT 227
DB 447 TCTCTTCATTCACCTCCATCTACAGCTGATGACACCCCTAAGTACACGGCTGCTACCT 388
QY 228 GTGGGTGTTTGGATCTATCGGAACCTCATTTGGAAGTGTGCACCTTTTTCATCTCTAC 287
DB 387 GTGGGTGTTTGGATCTATCGGAACCTCATTTGGAAGTGTGCACCTTTTTCATCTCTAC 328
QY 288 CCTCATTTGCTAATCATCATCTATCTTTACTGCGAGATCAGAGGGAAGGAAATTAT 347
DB 327 CCTCATTTGCTAATCATCATCTATCTTTACTGCGAGATCAGAGGGAAGGAAATTAT 268
QY 348 GATTAAGGCTGCTCCATGAGCAGATCATTAATGAGGCAAAAGATTAATGTTCTGATGCA 407
DB 267 GATTAAGGCTGCTCCATGAGCAGATCATTAATGAGGCAAAAGATTAATGTTCTGATGCA 208
QY 408 AAAATTGATCAAGCTGACGATATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGA 467
DB 207 AAAATTGATCAAGCTGACGATATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGA 148
QY 468 AAGGAGAGAGGTGAGCAACAAGCTTTTTCATTTGGGGAACATGATGGCAGTCTTGA 527
DB 147 AAGGAGAGAGGTGAGCAACAAGCTTTTTCATTTGGGGAACATGATGGCAGTCTTGA 88
QY 528 CTTCGATCTAGAGATCAGTTCAAGAAGGTAATCCAAAGGCC 570
DB 87 CTTCGATCTAGAGATCAGTTCAAGAAGGTAATCCAAAGGCC 45

RESULT 15
AW469181/c 594 bp mRNA linear EST 24-FEB-2000
LOCUS AW469181
DEFINITION hc78f11.x1 NCI-CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2898861 3'
similar to TR:043284 O43284 LAR-4P.; mRNA sequence.
ACCESSION AW469181
VERSION AW469181.1 GI:7039287
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 594)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/brp/image/image.html

Seq primer: -400P from Gibco

High quality sequence stop: 404.

FEATURES

source

1. 594

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2898861"

/clone_lib="NCI-CGAP_Gas4"

/tissue_type="poorly differentiated adenocarcinoma with
signed ring cell features"

/lab_host="DH10B"

/note="Organ: stomach; Vector: pCMV-SPORT6; site_1: SalI;

site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.69 kb. Life Technologies catalog #:

11549-011"

BASE COUNT 161 a 139 c 108 g 186 t

ORIGIN

Query Match

Best Local Similarity 59.4%; Score 338.8; DB 10; Length 594;

Matches 340; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 229 TGGGTGTTTGTGATCTATGGAACCTCATGTGAAGTGTGACCTTCTTTTCATCCTCACC 288
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Db 594 TGGGTGTTGGAATCTATGGAACCTCATGTGAAGTGTGACCTTCTTTTCATCCTCACC 535
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QY 289 CTCATTGTCTAATCATCACTATCTTTACTGCGAGATCACAGAGGAAGGAAGATTATG 348
      |||||
Db 534 CTCATTGTCTAATCATCACTATCTTTACTGCGAGATCACAGAGGAAGGAAGATTATG 475
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QY 349 ATAAGCTGCTCCATGAGCAGATCAATTAATGAGGGCAAGATAAATGTTCTGATAGAA 408
      |||||
Db 474 ATAAGCTGCTCCATGAGCAGATCAATTAATGAGGGCAAGATAAATGTTCTGATAGAA 415
      |||||

QY 409 AATTGATCAAGCTGACAGATATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAA 468
      |||||
Db 414 AATTGATCAAGCTGACAGATATGAGAGAAAGCAAAACCCAGCTCACTTGTCTGGAA 355
      |||||

QY 469 AGGAGAGAGGTGGAGCAACAGGCTTTTTCATTTGGGGGAACATGATGGCAGTCTTGAC 528
      |||||
Db 354 AGGAGAGAGGTGGAGCAACAGGCTTTTTCATTTGGGGGAACATGATGGCAGTCTTGAC 295
      |||||

QY 529 TTGCGATCTAGAAGATCACTTCAAGAAGTAATCCAAGGCC 570
      |||||
Db 294 TTGCGATCTAGAAGATCACTTCAAGAAGTAATCCAAGGCC 253
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Job time : 2224 secs

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